

FIG.-1A

5 P  
 6 GGCTCTACTAAATATTATCCATACTATACATTAATACAGAAATAATCTGCTATTTGGTATTCTGCAAATGAAAAAGGAGGAGGATTAAGA GTG  
 7  
 8 PRE  
 9 Arg Gly Lys Lys Val Thr Ile Ser Leu Leu Phe Ala Leu Ile Phe Thr Met Ala Phe Gly Ser Thr Ser  
 10 AGA GGC AAA AAA GIA TGG ATC AGT TCG CTC ATT GCT TTA ATC TTT ACG ATG GCG TTC GGC AGC ACA TCC  
 11  
 12 4 RBS  
 13 Met  
 14  
 15 PRO  
 16 Ser Ala Gin Ala Ala Gly Lys Ser Asn Gly Glu Lys Lys Tyr Ile Val Gly Phe Lys Glu Thr Met Ser Thr Met  
 17 TGT GGC CAG GCG GCA GGG AAA TCA AAC GGG GAA AAG AAA TAT ATT GTC GGG TTT AAA CAG ACA ATG AGC ACG ATG  
 18  
 19 Ser Ala Ala Lys Lys Asp Val Ile Ser Glu Lys Gly Lys Val Gly Lys Phe Lys Tyr Val Asp Ala  
 20 AGC GCC GCT AAC AAG AAA GAT GTC ATT TCT GAA AAA GCC GGG AAA GTG CAA AUG CAA TTC AAA TAT GTC GAC GCA  
 21  
 22 Ser Ala Ala Thr Leu Asn Glu Lys Ala Val Lys Glu Leu Lys Asp Pro Ser Val Ala Thr Val Glu Glu Asp  
 23 GCT TCA GCT ACA TTA AAC GAA AAA GCT GIA AAA GAA TTG AAA AAA GAC CGG AGC GTC GCT TAC GTT GAA GAA GAT  
 24  
 25 MAT  
 26 His Val Ala His Ala Thr Ala Gin Ser Val Pro Tyr Gly Val Ser Glu Ile Lys Ala Pro Ala Leu His Ser Glu  
 27 30 CAC GTC GCA CAT GCG TAC GCG CAG TCC GTG CCT TAC GCC GTC TCA TCA CAA ATT AAA GCC CCT CCT CTG CAC TCT CAA  
 28  
 29 Gly Thr Thr Gly Ser Asn Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val  
 30 GGC TAC ACT GGA TCA ATT GTC ATT GCA GCG GTT ATC GAC AGC GGT ATC GAT TCT CAT CCT GAT TCA AAG GTC

FIG. 1B - 1

FIG. - 1B - 2

1149 Gln Val Arg Ser Ser 250 Gln  
1149 CAA GAA GTC CGC AGC ACT TTA GAA AAC ACC ACT ACA AAA CTT GGT TAT GAT TCT TAC TAT GCA AAA GGG CTG ATC AAC  
1150 Val Gln Ala Ala 255  
1150 GAA GTC GCG GCA GCT CAG TAA AACATAAAAACGGGCTGGCCCGGGTTTTTATTTTCTCTGGATGTTCAATCCGCTCC

1156 ATAAATGGACGGATGGCTCCCTCTGAAAATTAAACGAGAAAACGGGGTGGACCCGGCTAGAGTCCCCTAACGGCCAAAGTCTGAAACGGTCGAATCCCG  
1156 CTTCCCGGTTCCGGTCACTCAATGCCGTACGGTACGGGGTTTCCCTGATAACGGGAGACGGCATTCGTAAATCCGATC

*FIG.-1B - 3*

*FIG.-1B - 1*

*FIG.-1B - 2*

*FIG.-1B - 3*

*FIG.-1B*

5435  
CONSERVED RESIDUES IN SUBTILISINS FROM  
BACILLUS AMYLOLIQUEFACIENS

1 10 20  
A Q S V P . G . . . . A P A . H . . G

21 30 40  
. T G S . V K V A V . D . G . . . . H P

41 50 60  
D L . . . G G A S . V P . . . . . Q D

61 70 80  
. N . H G T H V A G T . A A L N N S I G

81 90 100  
V L G V A P S A . L Y A V K V L G A . G

101 110 120  
S G . . S . L . . G . E W A . N . . . .

121 130 140  
V . N . S L G . P S . S . . . . A . .

141 150 160  
. . . . . G V . V V A A . G N . G . . .

161 170 180  
. . . . . Y P . . Y . . . . A V G A .

181 190 200  
D . . N . . A S P S . . G . . L D . . A

201 210 220  
P G V . . Q S T . P G . . Y . . . N G T

221 230 240  
S M A . P H V A G A A L . . . K . . .

241 250 260  
W . . . Q . R . . L . N T . . . L G . . .

261 270  
. . Y G . G L . N . . A A . . .

FIG.-2

COMPARISON OF SUBTILISIN SEQUENCES FROM:  
*B.amyloquefaciens*  
*B.subtilis*  
*B.licheniformis*  
*B.lentus*

60 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150

A Q S V P Y G V S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P	A Q S V P Y G I S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P	A Q T V P Y G I P L I K A D K V Q A Q G F K G A N V K V A V L D T G I Q A S H P	A Q S V P W G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T * H P
D L R V A G G A S H V P S E T N P F Q D N N S H G T H V A G T V A A L N N S I C	D L N V R G G A S P V P S E T N P Y Q D G S S H G T H V A G T I A A L N N S I C	D L N V V G G A S P V A G E A Y N * T D G G N G H G T H V A G T V A A L D N T T C	D L N I R G G A S P V P G E * P S T Q D G G N G H G T H V A G T I A A L N N S I C
V L G V A P S A S S L Y A V K V L G A D G S G Q Y S W I I N G I E W A I A N N M D	V L G V S P S A S S L Y A V K V L D S T G S G Q Y S W I I N G I E W A I S N N M D	V L G V A P S V S L Y A V K V L N S S G S G S Y S C I V S C I E W A T T N G M D	V L G V A P S A E L Y A V K V L G A S G S G S V S S I A Q G L E W A G N N G M R

FIG.\_3A

201	PGVSIQSTLPGN	210	PGN	220	SPH	230	H
	KYGAYNGTSM		KYGAYNGTSM		VAGAA		PN
	QSTLPGGTYGATP		QSTLPGGTYGATP		SPH		
	HTN		HTN		VAGAA		
	TYATLNGTSM		TYATLNGTSM		SPH		
	ASLNGTSM		ASLNGTSM		VAGAA		
	ATPHVAGAA		ATPHVAGAA		SPH		
	VAGAA		VAGAA		VAGAA		
	VAGAA		VAGAA		VAGAA		

241 WTNTQVRSSENTTKLGDSFYYCKGLINVQAAAQ  
242 WTNAQVRDLESSTATYLGNSFYYCKGLINVQAAAQ  
243 LSAASQVRNRLSSTATYLGSSFYYCKGLINVQAAAQ  
244 WGNVOLRNHLKNTATSLSGSTNLYGSSGLVNAEAATR  
245 250 255 260 265 270

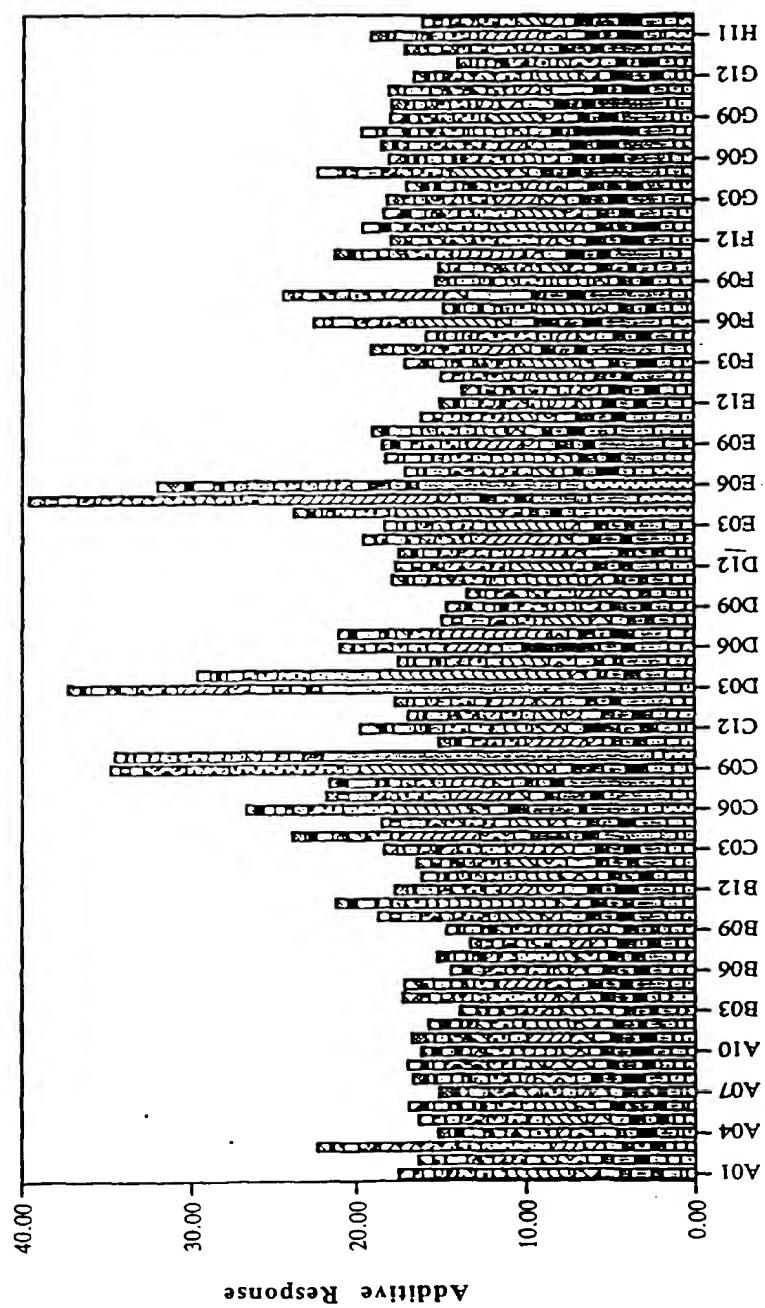
FIG. 3A

FIG. 3B

FIG. 3

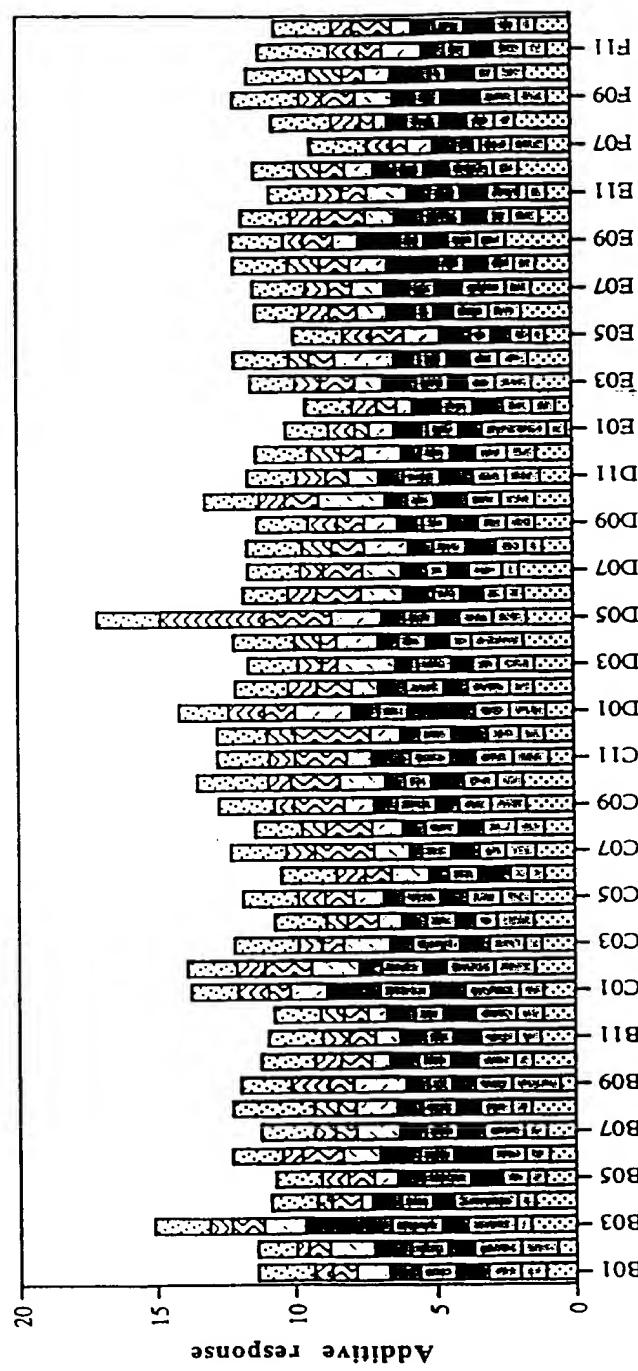
## FIG.\_3B

FIG. 4



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FIG. 5



Ney 25

1	A12	IKDFHVYFRESRDAG	49	E12	SATSRGVLVVAASGN
2	A11	LEQAVNSATSRGVLV	50	E11	SRGVLVVAASGNSGA
3	A10	AQSVPWGISRQVQAPA	51	E10	VLVVAASGNSGAGSI
4	A9	VPWGISRQAPAAHNGL	52	E9	VAASGNSGAGSISYP
5	A8	GISRVQAPAAHNRLG	53	E8	SGNSGAGSISYPARY
6	A7	RVQAPAAHNRLGTGS	54	E7	SGAGSISYPARYANA
7	A6	APAAHNRLGTGSVVK	55	E6	GSISYPARYANAMAV
8	A5	AHNRLGTGSVVKVAV	56	E5	SYPARYANAMAVGAT
9	A4	RGLTGSGVVKVAVLDT	57	E4	ARYANAMAVGATDQN
10	A3	TGSGVVKVAVLDTGIS	58	E3	ANAMAVGATDQNNR
11	A2	GVKVAVLDTGISTHP	59	E2	MAVGATDQNNNRASF
12	A1	VAVLDTGISTHPDLN	60	E1	GATDQNNNRASFSQL
13	B12	LDTGISTHPDLNIRG	61	F12	DQNNNRASFSQLYQAG
14	B11	GISTHPDLNIRGGAS	62	F11	NNRASFSQLYQAGLDI
15	B10	THPDLNIRGGASFVP	63	F10	ASFSQYQAGLDIVAP
16	B9	DLNIRGGASFVPGEPE	64	F9	SQYQAGLDIVAPGVN
17	B8	IRGGASFVPGEPESTQ	65	F8	GAGLDIVAPGVNVQS
18	B7	GASFVPGEPESTQDGN	66	F7	LDIVAPGVNVQSTYP
19	B6	FVPGEPESTQDGNHG	67	F6	VAPGVNVQSTYPGST
20	B5	GEPESTQDGNHGHTHV	68	F5	GVNVQSTYPGSTYAS
21	B4	STQDGNHGHTHVAGT	69	F4	VQSTYPGSTYASLNG
22	B3	DGNHGHTHVAGTIAA	70	F3	TYPGSTYASLNGTSM
23	B2	GHGHTHVAGTIAALNN	71	F2	GSTYASLNGTSMATP
24	B1	THVAGTIAALNNSIG	72	F1	YASLNGTSMATPHVA
25	C12	AGTIAALNNSIGVLG	73	G12	LNGTSMATPHVAGAA
26	C11	IAALNNSIGVLGVAP	74	G11	TSMATPHVAGAAALV
27	C10	LNNNSIGVLGVAPSAE	75	G10	ATPHVAGAAALVKQK
28	C9	SIGVLGVAPSAELYA	76	G9	HVAGAAALVKQKNPS
29	C8	VLGVAPSAELYAVKV	77	G8	GAAALVKQKNPSWSN
30	C7	VAPSAELYAVKVLGA	78	G7	ALVKQKNPSWSNVQI
31	C6	SAELYAVKVLGASGS	79	G6	KQKNPSWSNVQIRNH
32	C5	LYAVKVLGASGSGSV	80	G5	NPSWSNVQIRNHKLN
33	C4	VKVLGASGSGSVSSI	81	G4	WSNVQIRNHKNTAT
34	C3	LGASGSGSVSSIAQG	82	G3	VQIRNHKNTATSLG
35	C2	SGSGSVSSIAQGLEW	83	G2	RNHKNTATSLGSTN
36	C1	GSVSSIAQGLEWAGN	84	G1	LKNTATSLGSTNLYG
37	D12	SSIAQGLEWAGNNGM	85	H12	TATSLGSTNLYGSGL
38	D11	AQGLEWAGNNGMHVA	86	H11	SLGSTNLYGSGLVNA
39	D10	LEWAGNNGMHVA	87	H10	STNLYGSGLVNAEAA
40	D9	AGNNGMHVANL	88	H9	NLYGSGLVNAEATR
41	D8	SLGS			
42	D7	NGMHVANL			
43	D6	SLGS			
44	D5	PSAT			
45	D4	PSAT			
46	D3	PSAT			
47	D2	PSAT			
48	D1	PSAT			

FIG. 6A

11-4 35

1	A12	IKDFHVYFRESRDAG	49	E12	KKIDVLNLSIGGPDF
2	A11	DAELHIFRVFTNNQV	50	E11	DVLNLSIGGPDFMDH
3	A10	PLRRASLSLGSGFWH	51	E10	NLSIGGPDFMDHPFV
4	A9	RASLSLGSGFWHATG	52	E9	IGGPDFMDHPFVDKV
5	A8	LSLGSGFWHATGRHS	53	E8	PDFMDHPFVDKVWEL
6	A7	GSGFWHATGRHSSRR	54	E7	MDHPFVDKVWELTAN
7	A6	FWHATGRHSSRLLR	55	E6	PFVDKVWELTANNVI
8	A5	ATGRHSSRLLRAIP	56	E5	DKVWELTANNVIMVS
9	A4	RHSSRLLRAIPRQV	57	E4	WELTANNVIMVSAIG
10	A3	SRRLLRAIPRQVAQT	58	E3	TANNVIMVSAIGNDG
11	A2	LLRAIPRQVAQTLQA	59	E2	NVIMVSAIGNDGPLY
12	A1	AIPRQVAQTLQADVL	60	E1	MVSAIGNDGPLYGTJ
13	B12	RQVAQTLQADVLWQM	61	F12	AIGNDGPLYGTLN
14	B11	AQTLQADVLWQMGT	62	F11	NDGPLYGTLN
15	B10	LQADVLWQMGTGAN	63	F10	NDGPLYGTLN
16	B9	DVLWQMGTGANVRV	64	F9	NDGPLYGTLN
17	B8	WQMGTGANVRVAVF	65	F8	NDGPLYGTLN
18	B7	GYTGANVRVAVFDTG	66	F7	NDGPLYGTLN
19	B6	GANVRVAVFDTGLSE	67	F6	NDGPLYGTLN
20	B5	VRVAVFDTGLSEKHP	68	F5	NDGPLYGTLN
21	B4	AVFDTGLSEKHPFK	69	F4	NDGPLYGTLN
22	B3	DTGLSEKHPFKNVK	70	F3	NDGPLYGTLN
23	B2	LSEKHPFKNVKERT	71	F2	NDGPLYGTLN
24	B1	KHPFKNVKERTNWT	72	F1	NDGPLYGTLN
25	C12	HFKNVKERTNWTNER	73	G12	NDGPLYGTLN
26	C11	NVKERTNWTNERLTD	74	G11	NDGPLYGTLN
27	C10	ERTNWTNERLTDGL	75	G10	NDGPLYGTLN
28	C9	NWTNERLTDGLGHG	76	G9	NDGPLYGTLN
29	C8	NERLTDGLGHGTFV	77	G8	NDGPLYGTLN
30	C7	TLDDGLGHGTFVAGV	78	G7	NDGPLYGTLN
31	C6	DGLGHGTFVAGVIAS	79	G6	NDGPLYGTLN
32	C5	GHGTFVAGVIASMRE	80	G5	NDGPLYGTLN
33	C4	TFVAGVIASMRECQG	81	G4	NDGPLYGTLN
34	C3	AGVIASMRECQGFAP	82	G3	NDGPLYGTLN
35	C2	IASMRECQGFAPDAE	83	G2	NDGPLYGTLN
36	C1	MRECQGFAPDAELHI	84	G1	NDGPLYGTLN
37	D12	CQGFAPDAELHI	85	H12	NDGPLYGTLN
38	D11	FAPDAELHI	86	H11	NDGPLYGTLN
39	D10	DAELHIFRVFTNNQV	87	H10	NDGPLYGTLN
40	D9	LHIFRVFTNNQVSYT	88	H9	NDGPLYGTLN
41	D8	FRVFTNNQVSYTSWF	89	H8	NDGPLYGTLN
42	D7	FTNNQVSYTSWF	90	H7	NDGPLYGTLN
43	D6	NQVSYTSWF	91	H6	NDGPLYGTLN
44	D5	SYTSWF	92	H5	NDGPLYGTLN
45	D4	SWFLDAFN	93	H4	NDGPLYGTLN
46	D3	DAFN	94	H3	NDGPLYGTLN
47	D2	FNYAILKKIDVL	95	H2	NDGPLYGTLN
48	D1	AILKKIDVL	96	H1	NDGPLYGTLN

FIG. 6B

12 4 33

97	I12	IKDFHVYFRESRDAG
98	I11	DAELHIFRVFTNNQV
99	I10	KQALIASARRLPGVN
100	I9	LIASARRLPGVNMFE
101	I8	SARRLPGVNMFEQGH
102	I7	RLPGVNMFEQGHGKL
103	I6	GVNMFEQGHGKLDLL
104	I5	MFEQGHGKLDLLRAY
105	I4	QGHGKLDLLRAYQIL
106	I3	GKLDLLRAYQILNSY
107	I2	DLLRAYQILNSYKPQ
108	I1	RAYQILNSYKPQASL
109	J12	QILNSYKPQASLSPS
110	J11	NSYKPQASLSPSYID
111	J10	KPQASLSPSYIDLTE
112	J9	ASLSPSYIDLTECPY
113	J8	SPSYIDLTECPYMW
114	J7	YIDLTECPYMWPYCS
115	J6	LTECPYMWPYCSQPI
116	J5	CPYMWPYCSQPIYYG

FIG. 6C

1343

MKLVNIWLLLLVLLCGKKHLGDRLEKKSF EKAPCPGCSHLTLKVEFSSTVVEYEYIVAFNGYFT  
AKARNSFISSALKSSEVDNWRIIPRNNPSSDYPDFEVIQIKEKQAGLLTLEDHPNIKRVTPQR  
KVFRSLKYAESDPTVPCNETRWSQKWQSSRPLRRASLSLGSGFWHATGRHSSRLLRAIPRQVAQ  
TLQADVLWQMGTGANVRVAVFDTGLSEKHPFKNVKERTNWTNERTLDDGLGHGTAVGVIASM  
RECQGFAPDAELHIFRVFTNNQVSYTSWFLDAFNYAIIKKIDVLNLSIGGPDFMDHPFVDKVWEL  
TANNVIMVSAIGNDGPLYGTLLNPADQMDVIGVGGIDFEDNIARFSSRGMTTWELPGGYGRMKPD  
IVTYGAGVRGSGVKGGCRALSGTSAVSPVVAAGVTLVSTVQKRELVNPASMKQALIASARRLPG  
VNMFEOQGHGKLDLLRAYQILNSYKPQASLSPSYIDLTECPYMWPYCSPQIYYGGMPTVNNVTILN  
GMGVTRGRIVDKPDWQPYLPQNGDNEVAFSYSSVLWPWSGYLAISISVTKKAASWEGLAQGHVMI  
TVASPAETESKNGAEQTSTVLPKVKIIPTPPRSKRVLWDQYHNLRYPPGYFPDRNLRMKNDPL  
DWNGDHIHTNFRDMDYQHLRSMGYFVEVLGAPFTCFDASQYGTLLMVDSEEEYFPEEIAKLRRDVD  
NGLSLVIIFSDWYNTSVMRKVKFYDENTRQWWMPDTGGANI PALNELLSVWNMGFS DGLYEGEFTL  
ANHDMDYYASGCSIAKFPEDGVVITQTFKDQGLEVLKQETAVVENVPILGLYQIPAEGGGGRIVLYG  
DSNCLEDDSHRQKDCFWLLDALLQYTSYGVTPPSLSHSGNRQRPPSGAGSVT PERMEGNHLHRYSK  
VLEAHLGDPKPRPLPACPRLSWAKPQPLNETAPSNLWKHQKLLSIDLDKVVLPNFRSNRPQVRPL  
SPGESGAWDIPGGIMPGRYNQEVGQTIPVFAFLGAMVLAFFVUQINKAKSRPKRRKPRVKRPQL  
MQQVHPPKTPSV

FIG. 7

14 4 33

	10	20	30	40	50		
BPN'	AQSVPYGVSQ-IKAPALHSQGYTGSNVKVAVIDSGIDSSH	PDLK-VAGGA	48				
SAVINASE	AQSVPWGISR-VQAPAAHNRLTGSGVKVAVLDTG	I-STHPDLN-IRGGA	47				
S2HSBT	-RAI PRQVAQTLQADVLWQMGTG	ANVRVAVFDTGLSEKHPFKNVKERT	49				
	60	70	80	90	100		
BPN'	SMVPSETNPFQDNNSHGTHVAGTVAA	LNN SIGVLGVAPSASLYAVKV	LGA	98			
SAVINASE	SFVPGEPEST-QDGNGHGTHVAGTIA	ALNN SIGVLGVAPS	SAELYAVKV	LGA	96		
S2HSBT	NW-TNERTLDDGLGHGTFVAGVIAS	MRECQGF	APDAELHIFRVFTN		94		
	110	120	130	140	150		
BPN'	DGSGQYSWIIINGIEWAIAN	NMDVINMSLGGPS-GSAALKAA	VDKAVASGV	147			
SAVINASE	SGSGSVSSIAQGLEWAGNN	MHVANL	SLGSPS-PSATLEQAVNSATSRGV	145			
S2HSBT	NQVSYTSWFLDAFNYA	ILKKIDVLNL	SIGGPDFMDHPFVDKV	WELTANNV	144		
	160	170	180	190	200		
BPN'	VVVAAGNEGTS	GSSSTVGYPGK	KYPSVIAVGAVDSSNQRAS	FSSVGPEL-	197		
SAVINASE	LVVAASGNSGA	GSISYPARYANAMAVGATD	QNNNRASFSQY	GAGL-	191		
S2HSBT	IMVSAIGNDGP	QMDVIGVGGIDFEDNIARF	SSRGMT	TW	192		
	210	220	230	240	250		
BPN'	-----DVMAPGVSIQ	STLPGNKYGAYNGT	SMASPHVAGAA	ALIL	235		
SAVINASE	-----DIVAPGVNVQ	STYPG	STYASLN	GTSMATPHVAGAA	ALVK	229	
S2HSBT	ELPGGYGRMKPDI	VTYGAGVR	SGVKGGC	RALSGTSV	ASPVVAGAV	TLV	242
	260	270	280	290			
BPN'	SKHPNWTNTQ	VRSSLENT	TTKLGDSFY	YGKGLINVQAAAQ	275		
SAVINASE	QKNPSWSNVQ	IRNHLKNTAT	SLGSTNL	YGSGLVNAAEATR	269		
S2HSBT	STVQKRELVN	PASMKQALIASARR	LPGVNMFEQG	-----HGKL	280		

FIG. 8

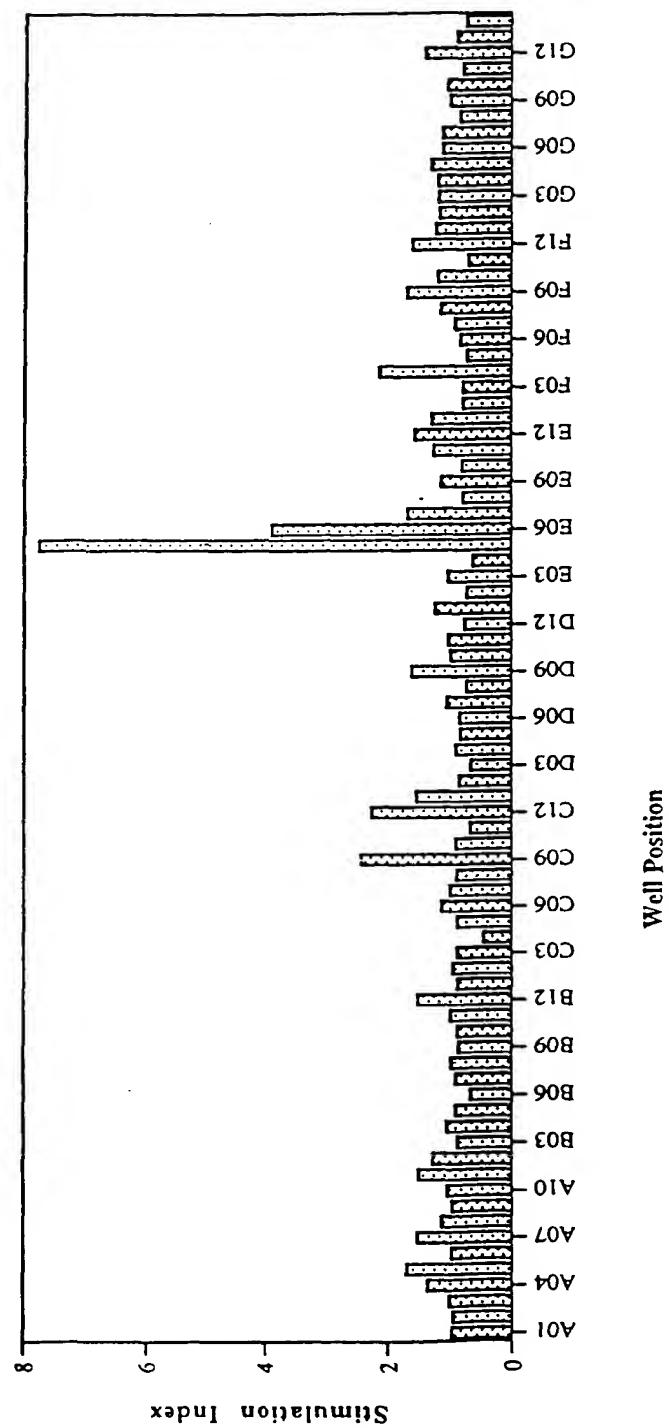
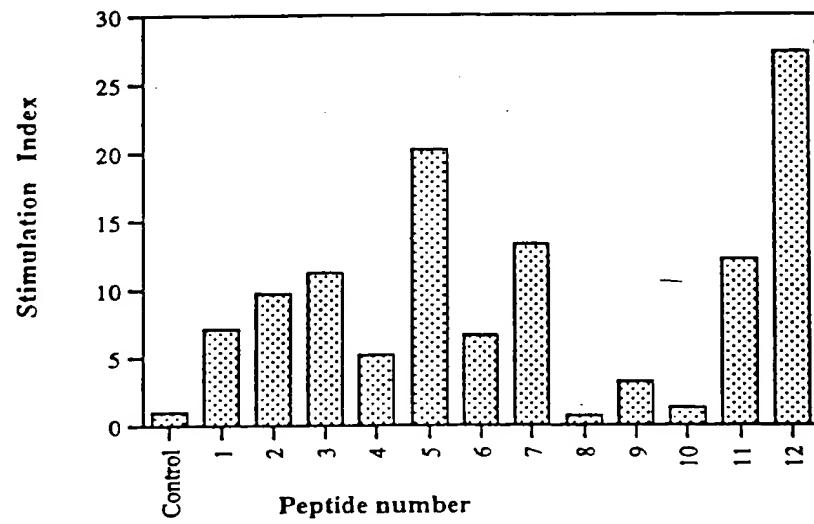


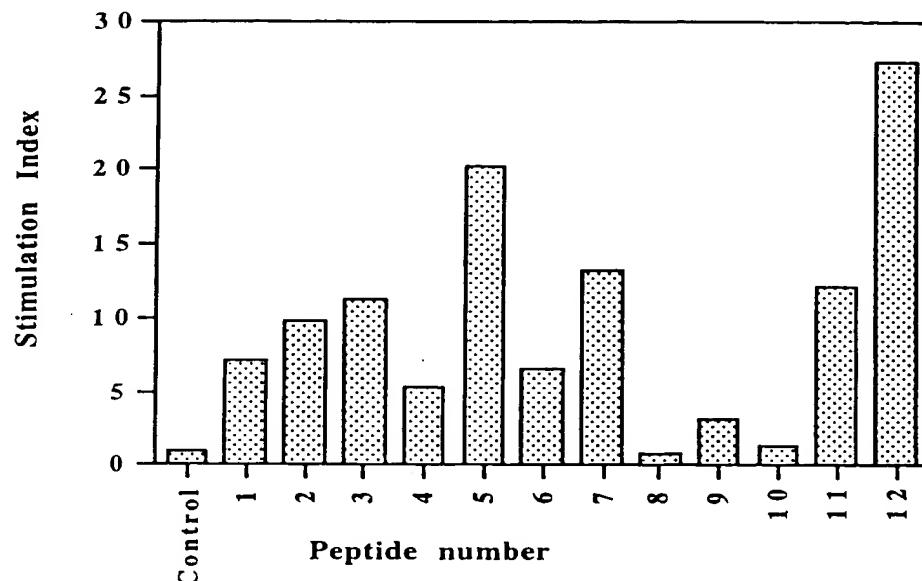
FIG. 9

10-435  
6



**FIG. 10**

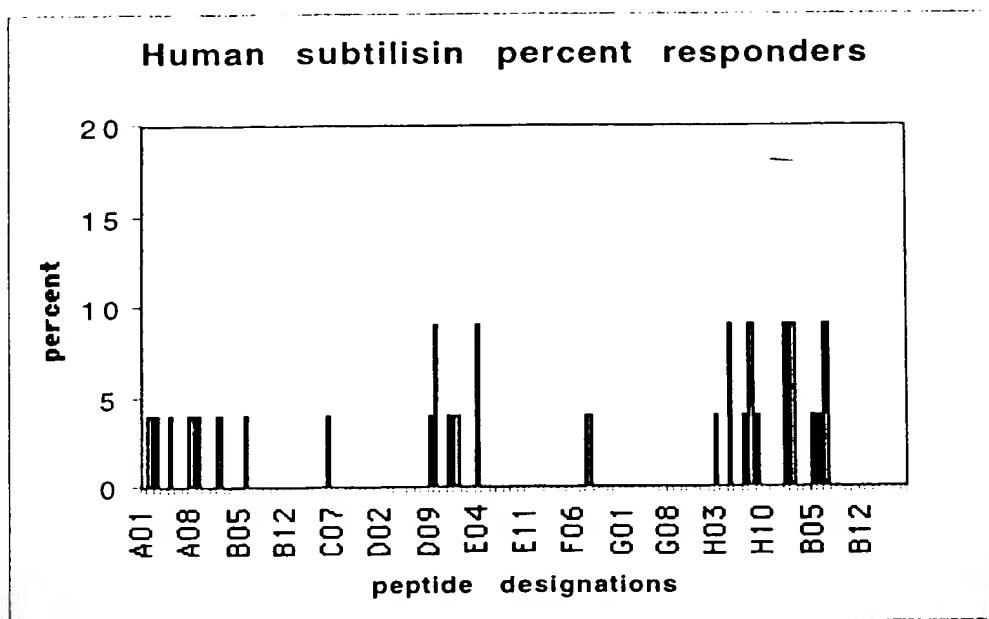
17 4/30



Peptide number	Sequence
1 (unmodified sequence)	GSISYPARYANAMAV
2	ASISYPARYANAMAV
3	GAISYPARYANAMAV
4	GSASYPARYANAMAV
5	GSIAYPARYANAMAV
6	GSISAPARYANAMAV
7	GSISYAARYANAMAV
8	GSISYPAAYANAMAV
9	GSISYPARAANAMAV
10	GSISYPARYAAAMAV
11	GSISYPARYANAAAV
12	GSISYPARYANAMAA

FIG. 11

18435



**FIG. 12**

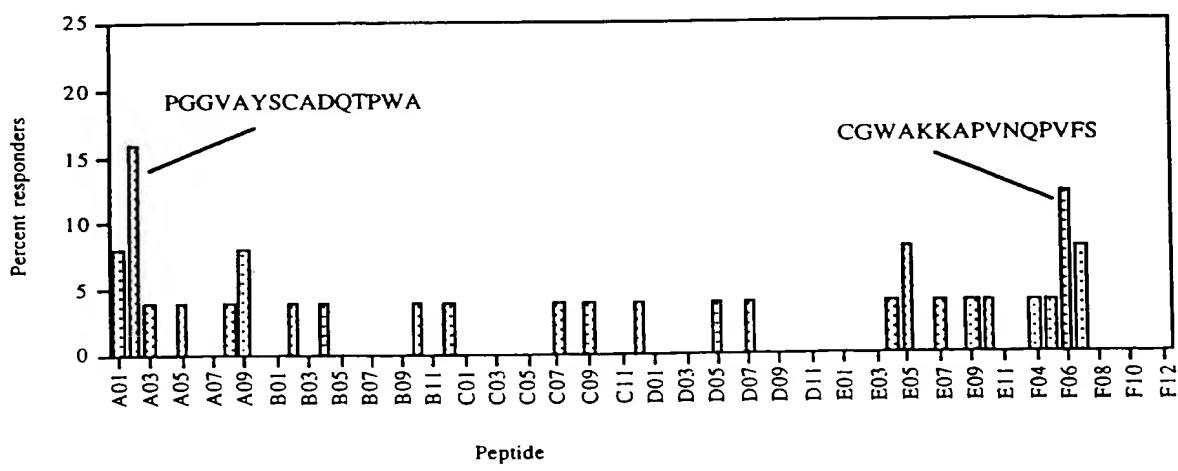


FIG. 13A

2 4 38

1	2	3	4	5
1234567890	1234567890	1234567890	1234567890	1234567890
MRSSPLLPSA	VVAALPVIAL	AADGRSTRYW	DCCKPSCGWA	<u>KKAPVNQPVF</u>
<u>SCNANFQRIT</u>	DFDAKSGCEP	<u>GGVAYSCADO</u>	<u>TPWAVNDdfa</u>	LGFAATSIAG
SNEAGWCCAC	YELTFTSGPV	AGKKMVVQST	STGGDLGSNH	FDLNIPGGGV
GIFDGCTPQF	GGLPGQRYGG	ISSRNECDRF	PDALKPGCYW	RFDWFKNADN
PSFSFRQVQC	PAELVARTGC	RRNDDGNFPA	VQIPSSSTSS	PVNQPTSTST
TSTSTTSSPP	VQPTTPSGCT	AERWAQ		

FIG. 13B

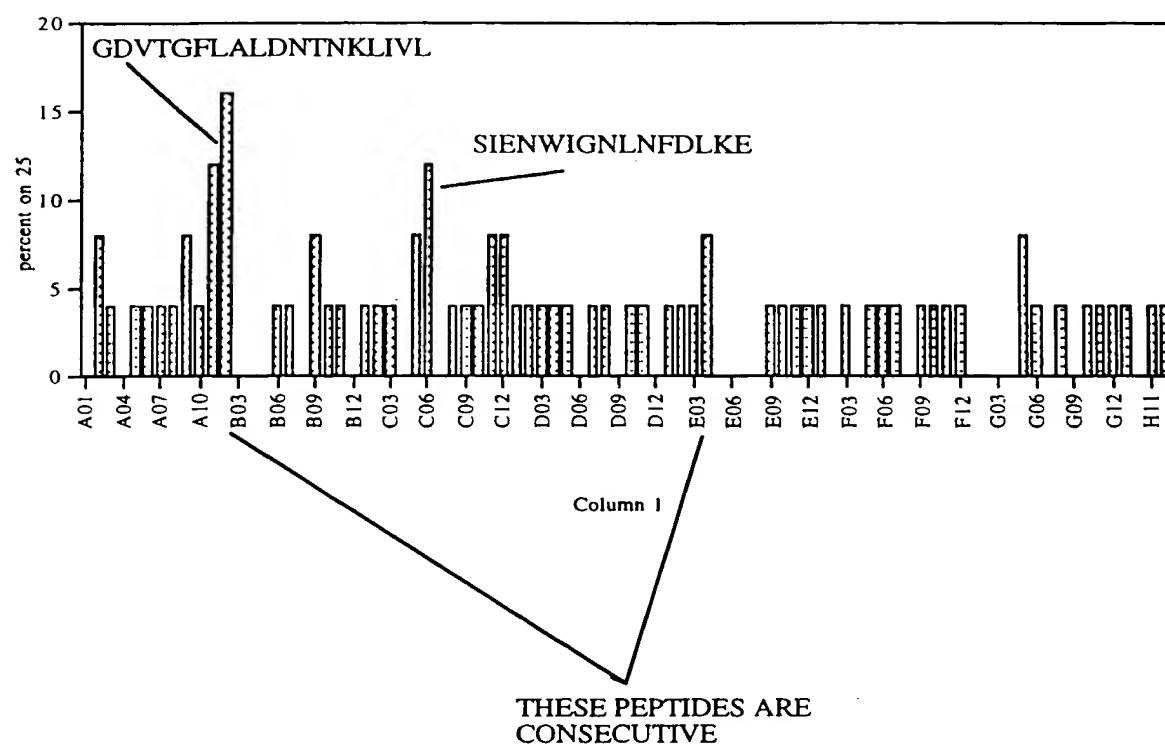
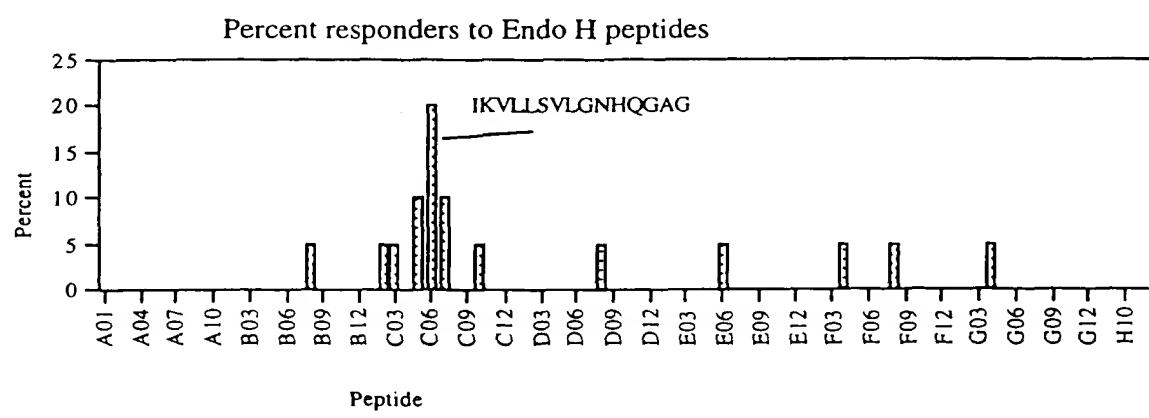


FIG. 14A

1 mrsslvlfv sawtalaspi rrevsqdlfn qfnlfaqysa aaycgknnda  
51 pagtnitctg nacpevekad atflysfeds **gvqdvtqfla** **ldntnklivl**  
101 sfrgsrsien **wignlnfdlk** eindicsgcr ghdgftsswr svadtlrqkv  
151 edavrehpdy rvvftghslg galatvagad lrgngydidv fsygaprvgn  
201 rafaefltvq tgglyrith tndivprlpp refgyshssp eywiksgtlv  
251 pvtrndivki egidatggnn qpnipdipah lwyfgligtc 1

FIG. 14B

**FIG. 15A**

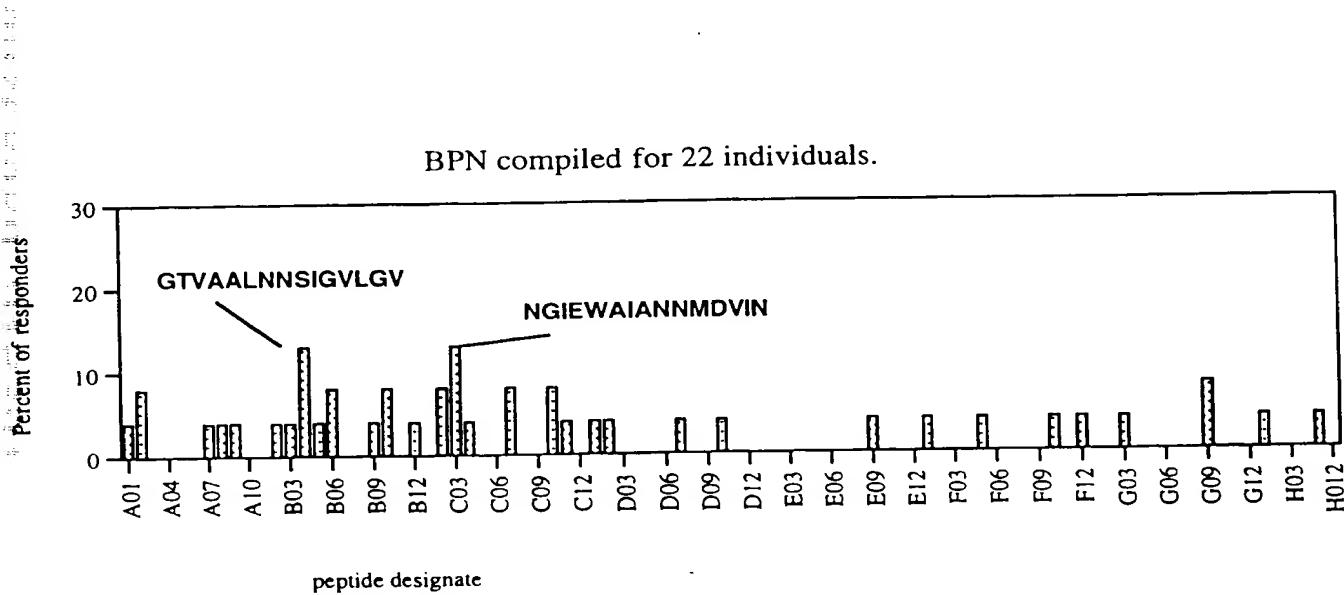
1 mftpvrrrvr taalalsaaa alvlgstaas gasatpspap apapapvkqg  
51 ptsvayvevn nnsmlnvkky tladgggnaf dvavifaani nydtgtktay  
101 lhfnenvqrv ldnavtqirp lqqqgikvll svlgnhqqaq fanfpsqaa  
151 safakqlsda vakygldgvd ffdeyaeygn ngtaqpnndss fvhlvatalra  
201 nmpdkiisly nigpaasrls yggvdvsdkf dyawnpyygt wqvpgialpk  
251 aqlspaavei grtsrstvad larrtvdegy gvyltynldg gdrtadvsaf  
301 trelygseav rtp

**FIG. 15B**

25 of 35

25 of 35

BPN compiled for 22 individuals.



**FIG. 16**

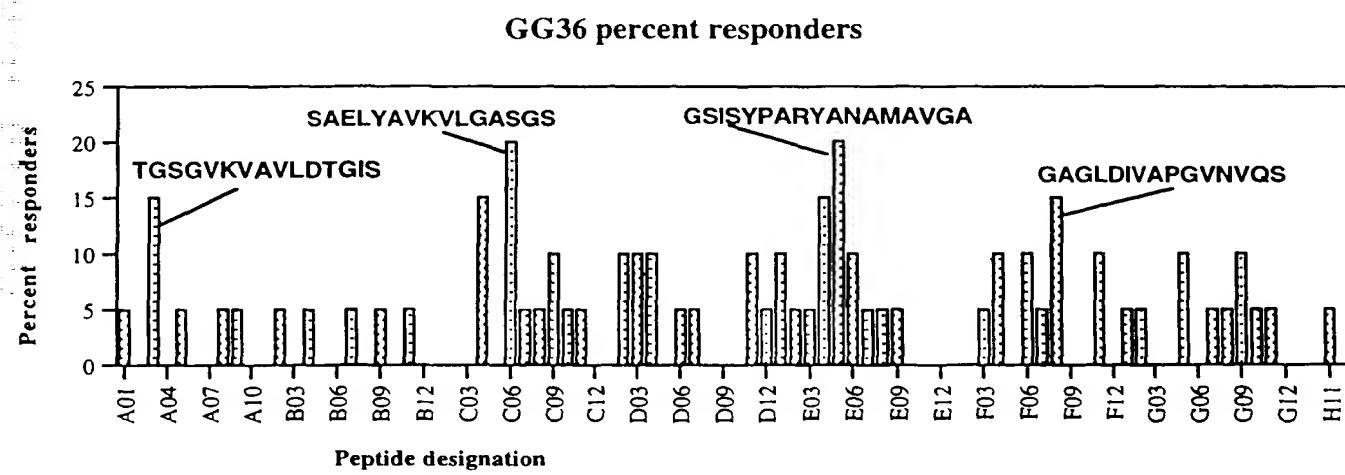


FIG. 17

## Hybrid enzyme sequence (GG36-BPN)

GG36

AQSVPWGISRVQAPAAHNRLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPESTQDGNGH

BPN

GTHVAGTIAALNNSIGVLGVAPS AELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVINMSLGGS

△

GSAALKAAVDKAVASGVVVVAAAGNEGTGSSSTVGYPGKYP SVIAVGAVDSSNQRASFSSVGP

ELDVMAPGVSIQSTLPGNKYGA YNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLNTT KLGD

SFYY GKGLINVQAAAQ

**FIG. 18**

45 + 35

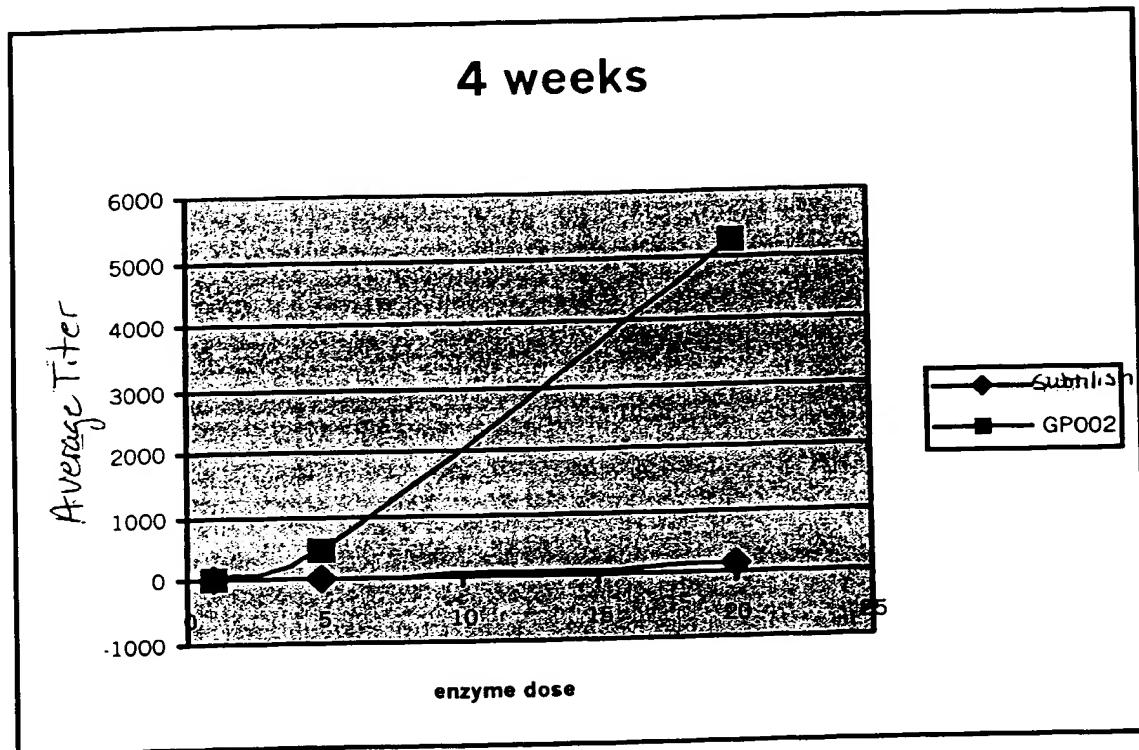


FIGURE 19A

29 4/35

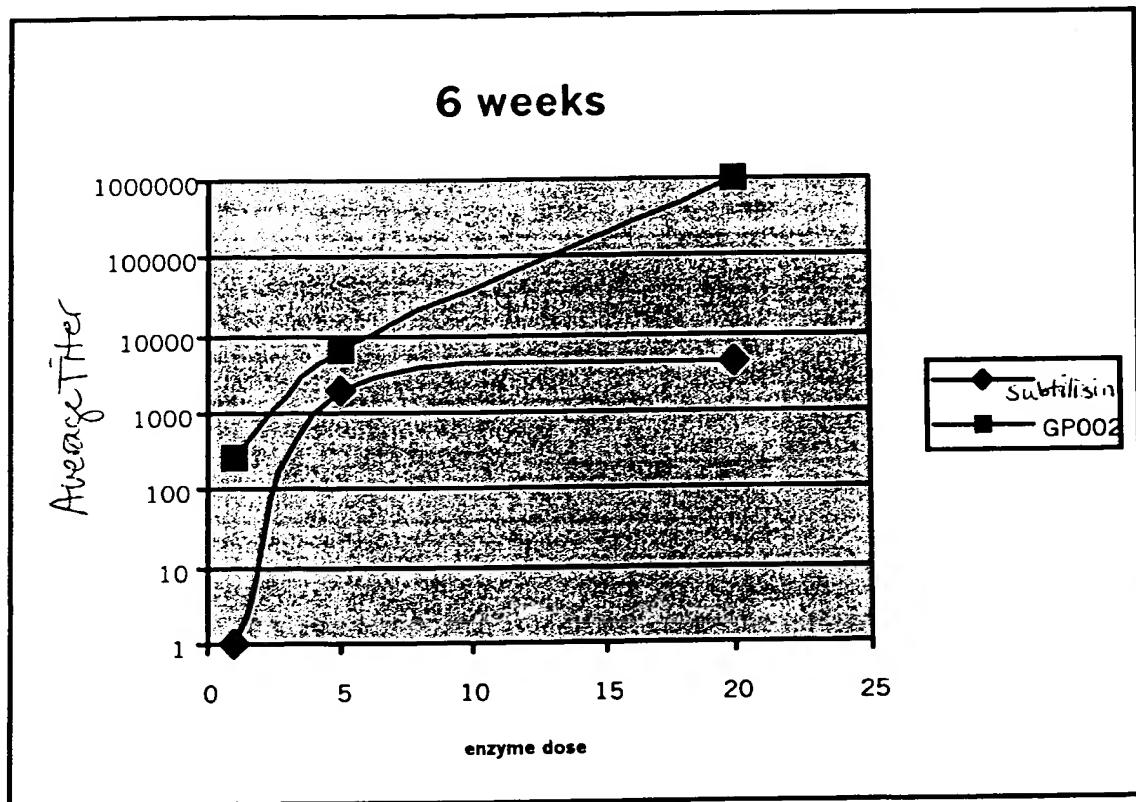
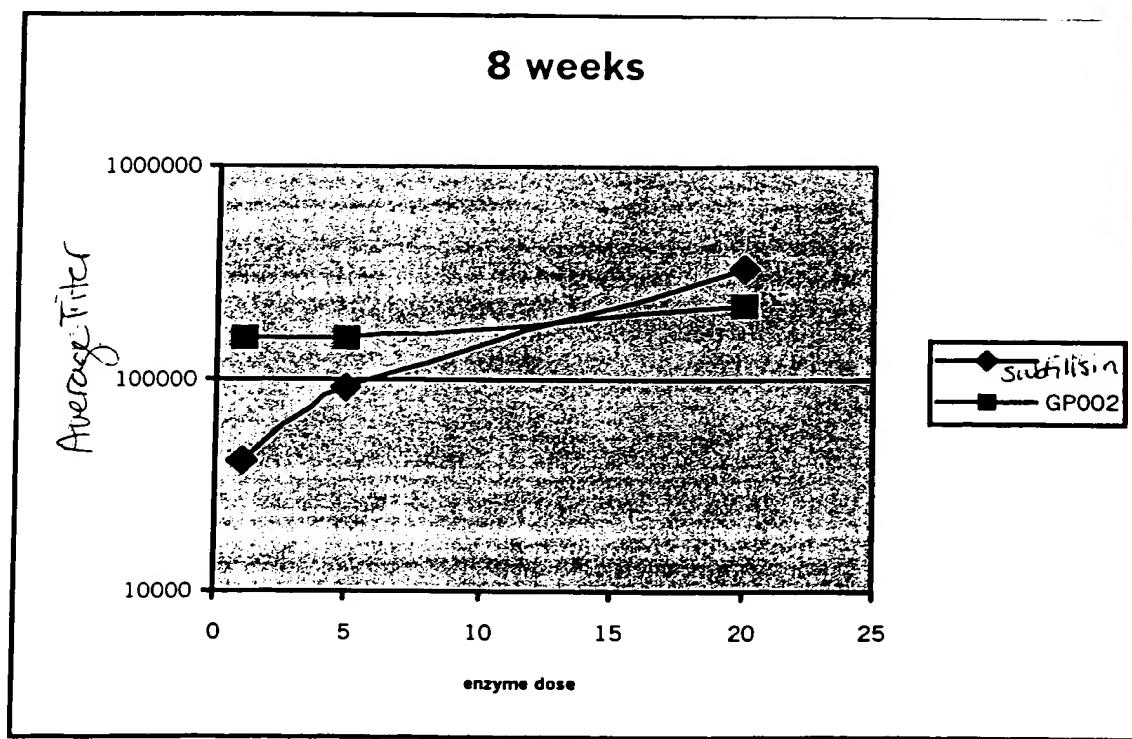
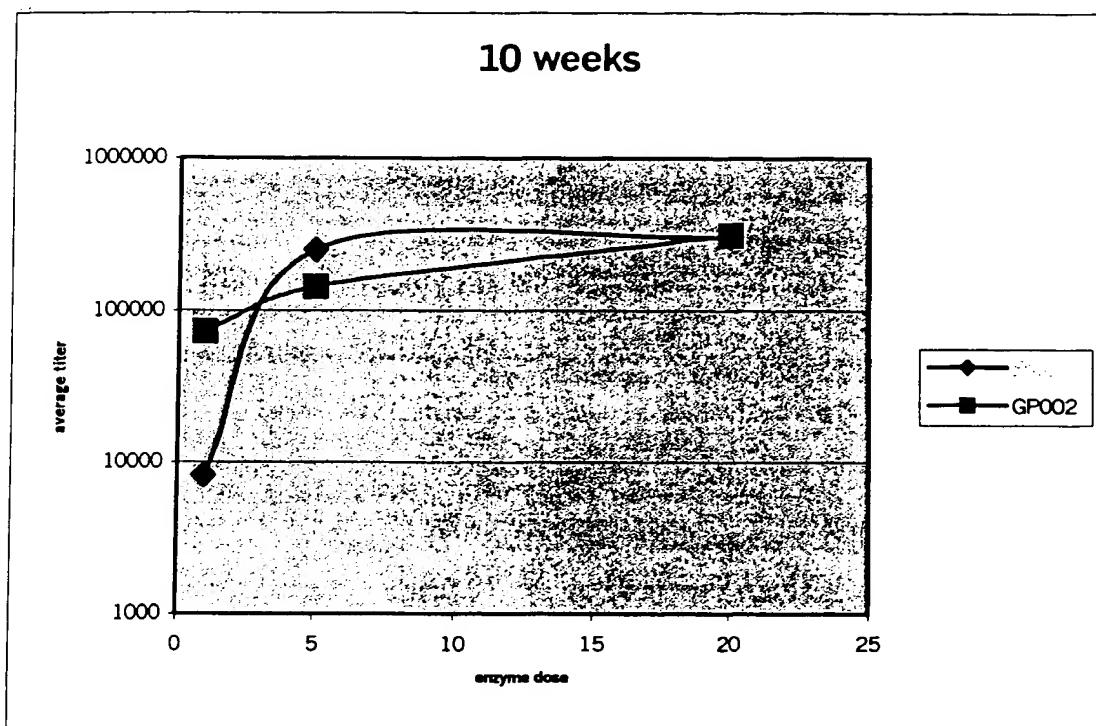


FIGURE 19B

30-435



**FIGURE 19C**



**FIGURE 19D**

32 of 35

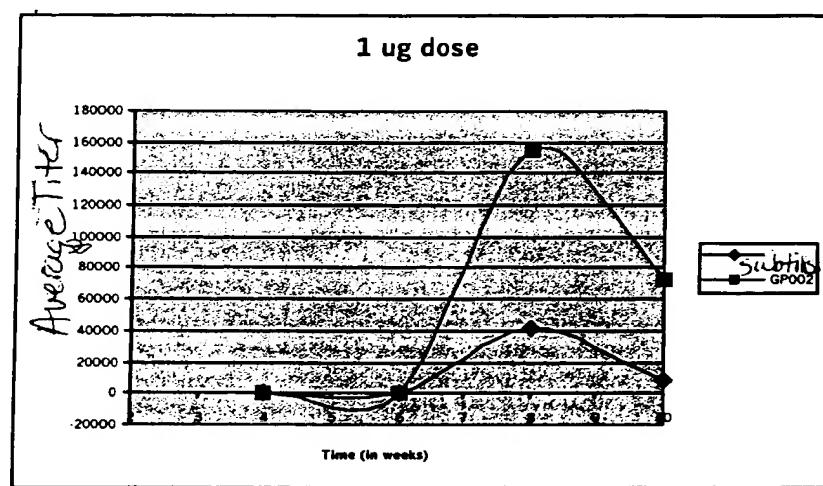


FIGURE 20A

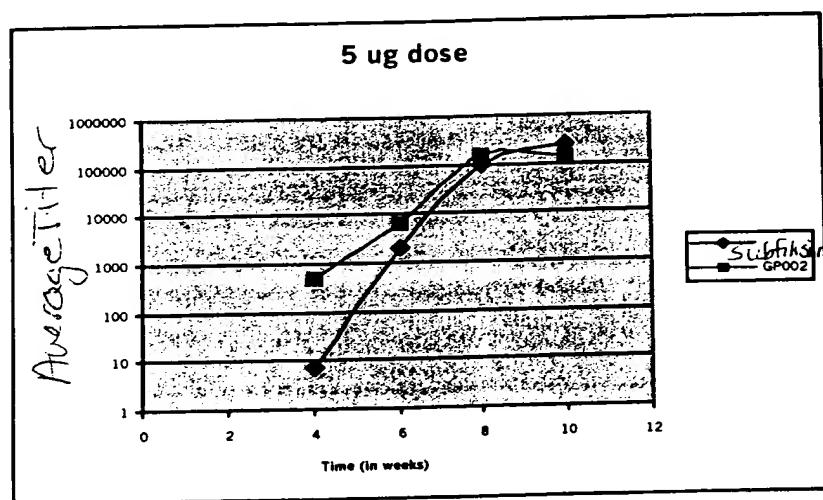


FIGURE 20B

44 35

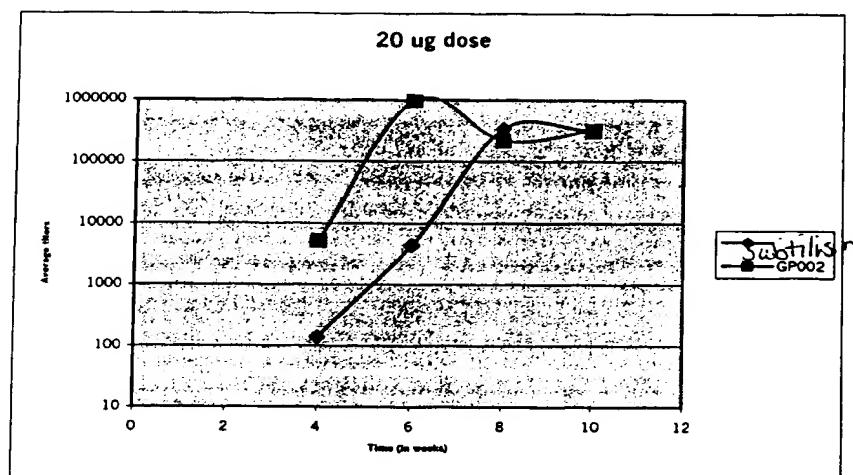
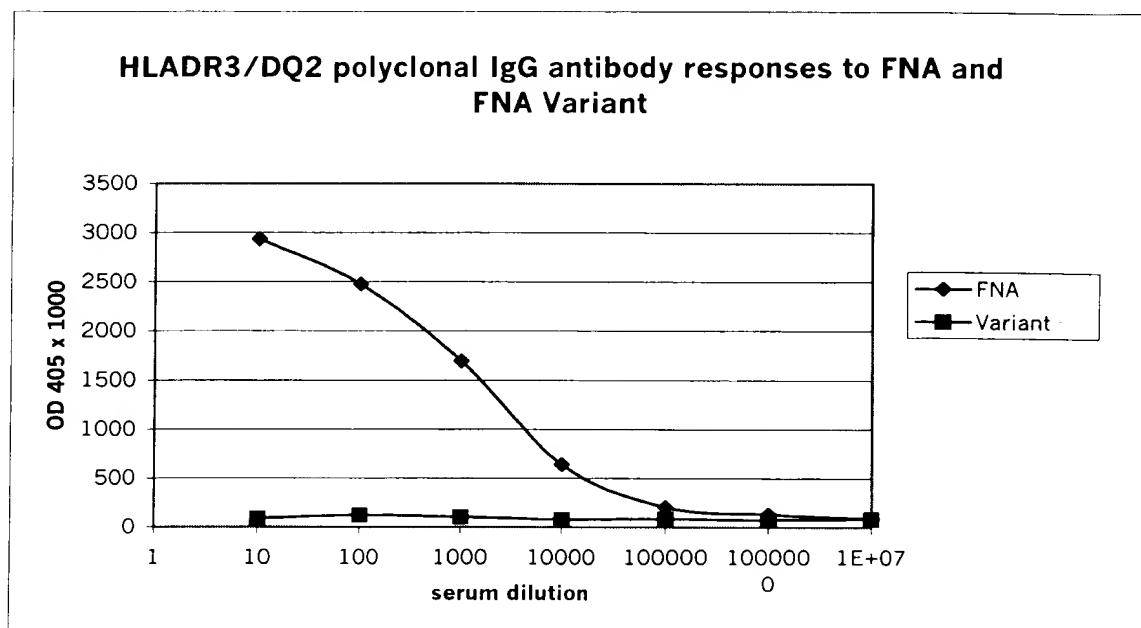


FIGURE 20C



**FIGURE 21**